

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Blinkovsky, Alexander
Berka, Randy
Rey, Michael
Golightly, Elizabeth
Klotz, Alan
Mathisen, Thomas Erik
Dambmann, Claus
- (ii) TITLE OF THE INVENTION: Carboxypeptidases And Nucleic Acids
Encoding Same
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Novo Nordisk of North America, Inc.
 - (B) STREET: 405 Lexington Avenue
 - (C) CITY: New York
 - (D) STATE: NY
 - (E) COUNTRY: USA
 - (F) ZIP: 10174
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: to be assigned
 - (B) FILING DATE: 03-OCT-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Lambiris, Elias J
 - (B) REGISTRATION NUMBER: 33,728
 - (C) REFERENCE/DOCKET NUMBER: 4990.200-US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 212-867-0123
 - (B) TELEFAX: 212-878-9655
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1662 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1662
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CGT GGC TAC GAA TTT CTC TCA GTG CTA CCC TTG GTT GCA GCC AGT	48
Met Arg Gly Tyr Glu Phe Leu Ser Val Leu Pro Leu Val Ala Ala Ser	
1 5 10 15	
TGG GCC CTT CCA GGA AGT ACA CCG GCG TCC GTC GGT AGA AGA CAG CTA	96
Trp Ala Leu Pro Gly Ser Thr Pro Ala Ser Val Gly Arg Arg Gln Leu	
20 25 30	
CCC AAG AAC CCC ACC GGG GTC AAG ACT CTT ACA ACC GCA AAC AAT GTC	144
Pro Lys Asn Pro Thr Gly Val Lys Thr Leu Thr Thr Ala Asn Asn Val	
35 40 45	
ACC ATC CGG TAC AAG GAA CCC GGG GCA GAG GGC GTC TGC GAG ACT ACC	192
Thr Ile Arg Tyr Lys Glu Pro Gly Ala Glu Gly Val Cys Glu Thr Thr	
50 55 60	
CCG GGT GTC AAA TCC TAC TCT GGA TAT GTC GAC ACC TCT CCC GAG TCC	240
Pro Gly Val Lys Ser Trp Ser Gly Tyr Val Asp Thr Ser Pro Glu Ser	
65 70 75 80	
CAT ACC TTC TTC TGG TTC TTC GAA GCC AGA CAT AAC CCA GAA ACT GCA	288
His Thr Phe Phe Trp Phe Phe Glu Ala Arg His Asn Pro Glu Thr Ala	
85 90 95	
CCT ATC ACA TTG TGG TTG AAT GGT GGC CCT GGA AGC GAT TCT TTG ATC	336
Pro Ile Thr Leu Trp Leu Asn Gly Gly Pro Gly Ser Asp Ser Leu Ile	
100 105 110	
GGT CTC TTC GAA GAG TTG GGC CCT TGC CAT GTC AAT TCG ACT TTT GAT	384
Gly Leu Phe Glu Glu Leu Gly Pro Cys His Val Asn Ser Thr Phe Asp	
115 120 125	
GAC TAC ATC AAC CCT CAC TCG TGG AAC GAG GTC TCC AAT TTA CTA TTC	432
Asp Tyr Ile Asn Pro His Ser Trp Asn Glu Val Ser Asn Leu Leu Phe	
130 135 140	
CTG TCC CAG CCA TTG GGA GTC GGC TTT TCA TAT AGT GAT ACG GTT GAT	480
Leu Ser Gln Pro Leu Gly Val Gly Phe Ser Tyr Ser Asp Thr Val Asp	
145 150 155 160	
GGG TCC ATT AAC CCT GTA ACT GGG GTC GTC GAA AAT TCG AGC TTT GCA	528
Gly Ser Ile Asn Pro Val Thr Gly Val Val Glu Asn Ser Ser Phe Ala	
165 170 175	
GGA GTT CAG GGC CGG TAC CCA ACC ATT GAT GCC ACT CTG ATC GAT ACT	576
Gly Val Gln Gly Arg Tyr Pro Thr Ile Asp Ala Thr Leu Ile Asp Thr	
180 185 190	
ACC AAT CTT GCC GCA GAG GCC GCT TGG GAG ATC CTG CAA GGA TTC CTT	624
Thr Asn Leu Ala Ala Glu Ala Ala Trp Glu Ile Leu Gln Gly Phe Leu	
195 200 205	
AGT GGA CTA CCT AGC TTG GAC TCT AGG GTG CAG TCT AAG GAC TTC AGT	672
Ser Gly Leu Pro Ser Leu Asp Ser Arg Val Gln Ser Lys Asp Phe Ser	
210 215 220	
CTA TGG ACG GAG AGC TAT GGA GGG CAC TAT GGT CCT GCA TTC TTC AAT	720
Leu Trp Thr Glu Ser Tyr Gly Gly His Tyr Gly Pro Ala Phe Phe Asn	
225 230 235 240	
CAT TTT TAC GAG CAG AAT GAG AGA ATT GCC AAC GGT AGT GTT AAT GGT	768
His Phe Tyr Glu Gln Asn Glu Arg Ile Ala Asn Gly Ser Val Asn Gly	
245 250 255	

GTT CAG CTT AAT TTC AAC TCT CTG GGA ATT ATT AAC GGC ATC ATC GAC	816
Val Gln Leu Asn Phe Asn Ser Leu Gly Ile Ile Asn Gly Ile Ile Asp	
260 265 270	
GAG GCG ATC CAG GCC CCT TAC TAC CCT GAA TTC GCT GTG AAC AAT ACC	864
Glu Ala Ile Gln Ala Pro Tyr Tyr Pro Glu Phe Ala Val Asn Asn Thr	
275 280 285	
TAC GGT ATC AAG GCT GTC AAC GAG ACC GTC TAC AAC TAC ATG AAG TTT	912
Tyr Gly Ile Lys Ala Val Asn Glu Thr Val Tyr Asn Tyr Met Lys Phe	
290 295 300	
GCC AAC CAA ATG CCA AAT GGT TGC CAG GAT TTG ATT TCC ACC TGC AAA	960
Ala Asn Gln Met Pro Asn Gly Cys Gln Asp Leu Ile Ser Thr Cys Lys	
305 310 315 320	
CAG ACA AAC CGC ACC GCA TTA GCT GAC TAC GCC CTC TGC GCC GAA GCC	1008
Gln Thr Asn Arg Thr Ala Leu Ala Asp Tyr Ala Leu Cys Ala Glu Ala	
325 330 335	
ACC AAC ATG TGC AGG GAC AAT GTT GAG GGG CCA TAC TAC GCC TTT GCT	1056
Thr Asn Met Cys Arg Asp Asn Val Glu Gly Pro Tyr Tyr Ala Phe Ala	
340 345 350	
GGT CGT GGT GTG TAT GAT ATT CGG CAT CCA TAT GAT GAC CCG ACT CCG	1104
Gly Arg Gly Val Tyr Asp Ile Arg His Pro Tyr Asp Pro Thr Pro	
355 360 365	
CCA AGT TAT TAC AAC AAA TTT CTG GCA AAG GAC TCT GTC ATG GAC GCT	1152
Pro Ser Tyr Tyr Asn Lys Phe Leu Ala Lys Asp Ser Val Met Asp Ala	
370 375 380	
ATC GGC GTC AAC ATC AAC TAC ACC CAG TCC AAT AAT GAC GTC TAC TAC	1200
Ile Gly Val Asn Ile Asn Tyr Thr Gln Ser Asn Asn Asp Val Tyr Tyr	
385 390 395 400	
GCT TTC CAG CAA ACA GGC GAC TTT GTC TGG CCC AAC TTC ATC GAA GAC	1248
Ala Phe Gln Gln Thr Gly Asp Phe Val Trp Pro Asn Phe Ile Glu Asp	
405 410 415	
CTC GAG GAG ATC CTT GCT CTC CCC GTG CGT GTC TCC CTC ATC TAT GGC	1296
Leu Glu Glu Ile Leu Ala Leu Pro Val Arg Val Ser Leu Ile Tyr Gly	
420 425 430	
GAC GCC GAT TAC ATC TGC AAC TGG TTC GGC GGT CAG GCC GTT TCC CTC	1344
Asp Ala Asp Tyr Ile Cys Asn Trp Phe Gly Gly Gln Ala Val Ser Leu	
435 440 445	
GCT GCG AAC TAC TCC CAA GCC GCC CAG TTC CGA AGC GCA GGG TAC ACG	1392
Ala Ala Asn Tyr Ser Gln Ala Ala Gln Phe Arg Ser Ala Gly Tyr Thr	
450 455 460	
CCC CTG AAA GTC AAC GGC GTC GAG TAT GGG GAA ACT CGC GAG TAT GGT	1440
Pro Leu Lys Val Asn Gly Val Glu Tyr Gly Glu Thr Arg Glu Tyr Gly	
465 470 475 480	
AAT TTC TCC TTC ACT CGC GTC TAT GAG GCA GGC CAT GAA GTC CCA TAC	1488
Asn Phe Ser Phe Thr Arg Val Tyr Glu Ala Gly His Glu Val Pro Tyr	
485 490 495	
TAC CAG CCC ATC GCC TCC CTG CAA TTG TTT AAC CGG ACT ATC TTC GGT	1536
Tyr Gln Pro Ile Ala Ser Leu Gln Leu Phe Asn Arg Thr Ile Phe Gly	
500 505 510	
TGG GAT ATC GCA GAG GGC CAG AAG AAG ATC TGG CCC AGC TAC AAG ACG	1584
Trp Asp Ile Ala Glu Gly Gln Lys Lys Ile Trp Pro Ser Tyr Lys Thr	
515 520 525	

AAT GGA ACG GCT ACA GCT ACG CAT ACA CAG TCG TCC GTG CCG CTG CCT	1632
Asn Gly Thr Ala Thr Ala Thr His Thr Gln Ser Ser Val Pro Leu Pro	
530 535 540	
ACG GCT ACC AGC ATG TCC AGT GTT GGT ATG	1662
Thr Ala Thr Ser Met Ser Ser Val Gly Met	
545 550	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Gly	Tyr	Glu	Phe	Leu	Ser	Val	Leu	Pro	Leu	Val	Ala	Ala	Ser	1	5	10	15
Trp	Ala	Leu	Pro	Gly	Ser	Thr	Pro	Ala	Ser	Val	Gly	Arg	Arg	Gln	Leu	20	25	30	
Pro	Lys	Asn	Pro	Thr	Gly	Val	Lys	Thr	Leu	Thr	Thr	Ala	Asn	Asn	Val	35	40	45	
Thr	Ile	Arg	Tyr	Lys	Glu	Pro	Gly	Ala	Glu	Gly	Val	Cys	Glu	Thr	Thr	50	55	60	
Pro	Gly	Val	Lys	Ser	Tyr	Ser	Gly	Tyr	Val	Asp	Thr	Ser	Pro	Glu	Ser	65	70	75	80
His	Thr	Phe	Phe	Trp	Phe	Phe	Glu	Ala	Arg	His	Asn	Pro	Glu	Thr	Ala	85	90	95	
Pro	Ile	Thr	Leu	Trp	Leu	Asn	Gly	Gly	Pro	Gly	Ser	Asp	Ser	Leu	Ile	100	105	110	
Gly	Leu	Phe	Glu	Glu	Leu	Gly	Pro	Cys	His	Val	Asn	Ser	Thr	Phe	Asp	115	120	125	
Asp	Tyr	Ile	Asn	Pro	His	Ser	Trp	Asn	Glu	Val	Ser	Asn	Leu	Leu	Phe	130	135	140	
Leu	Ser	Gln	Pro	Leu	Gly	Val	Gly	Phe	Ser	Tyr	Ser	Asp	Thr	Val	Asp	145	150	155	160
Gly	Ser	Ile	Asn	Pro	Val	Thr	Gly	Val	Val	Glu	Asn	Ser	Ser	Phe	Ala	165	170	175	
Gly	Val	Gln	Gly	Arg	Tyr	Pro	Thr	Ile	Asp	Ala	Thr	Leu	Ile	Asp	Thr	180	185	190	
Thr	Asn	Leu	Ala	Ala	Glu	Ala	Ala	Trp	Glu	Ile	Leu	Gln	Gly	Phe	Leu	195	200	205	
Ser	Gly	Leu	Pro	Ser	Leu	Asp	Ser	Arg	Val	Gln	Ser	Lys	Asp	Phe	Ser	210	215	220	
Leu	Trp	Thr	Glu	Ser	Tyr	Gly	Gly	His	Tyr	Gly	Pro	Ala	Phe	Phe	Asn	225	230	235	240

His	Phe	Tyr	Glu	Gln	Asn	Glu	Arg	Ile	Ala	Asn	Gly	Ser	Val	Asn	Gly	
				245					250					255		
Val	Gln	Leu	Asn	Phe	Asn	Ser	Leu	Gly	Ile	Ile	Asn	Gly	Ile	Ile	Asp	
			260					265					270			
Glu	Ala	Ile	Gln	Ala	Pro	Tyr	Tyr	Pro	Glu	Phe	Ala	Val	Asn	Asn	Thr	
		275					280					285				
Tyr	Gly	Ile	Lys	Ala	Val	Asn	Glu	Thr	Val	Tyr	Asn	Tyr	Met	Lys	Phe	
	290					295					300					
Ala	Asn	Gln	Met	Pro	Asn	Gly	Cys	Gln	Asp	Leu	Ile	Ser	Thr	Cys	Lys	
305					310					315					320	
Gln	Thr	Asn	Arg	Thr	Ala	Leu	Ala	Asp	Tyr	Ala	Leu	Cys	Ala	Glu	Ala	
				325					330					335		
Thr	Asn	Met	Cys	Arg	Asp	Asn	Val	Glu	Gly	Pro	Tyr	Tyr	Ala	Phe	Ala	
			340					345					350			
Gly	Arg	Gly	Val	Tyr	Asp	Ile	Arg	His	Pro	Tyr	Asp	Asp	Pro	Thr	Pro	
		355					360					365				
Pro	Ser	Tyr	Tyr	Asn	Lys	Phe	Leu	Ala	Lys	Asp	Ser	Val	Met	Asp	Ala	
	370					375					380					
Ile	Gly	Val	Asn	Ile	Asn	Tyr	Thr	Gln	Ser	Asn	Asn	Asp	Val	Tyr	Tyr	
385					390					395					400	
Ala	Phe	Gln	Gln	Thr	Gly	Asp	Phe	Val	Trp	Pro	Asn	Phe	Ile	Glu	Asp	
				405					410					415		
Leu	Glu	Glu	Ile	Leu	Ala	Leu	Pro	Val	Arg	Val	Ser	Leu	Ile	Tyr	Gly	
			420					425					430			
Asp	Ala	Asp	Tyr	Ile	Cys	Asn	Trp	Phe	Gly	Gly	Gln	Ala	Val	Ser	Leu	
		435					440					445				
Ala	Ala	Asn	Tyr	Ser	Gln	Ala	Ala	Gln	Phe	Arg	Ser	Ala	Gly	Tyr	Thr	
		450				455					460					
Pro	Leu	Lys	Val	Asn	Gly	Val	Glu	Tyr	Gly	Glu	Thr	Arg	Glu	Tyr	Gly	
465					470					475					480	
Asn	Phe	Ser	Phe	Thr	Arg	Val	Tyr	Glu	Ala	Gly	His	Glu	Val	Pro	Tyr	
				485					490					495		
Tyr	Gln	Pro	Ile	Ala	Ser	Leu	Gln	Leu	Phe	Asn	Arg	Thr	Ile	Phe	Gly	
			500					505					510			
Trp	Asp	Ile	Ala	Glu	Gly	Gln	Lys	Lys	Ile	Trp	Pro	Ser	Tyr	Lys	Thr	
		515					520					525				
Asn	Gly	Thr	Ala	Thr	Ala	Thr	His	Thr	Gln	Ser	Ser	Val	Pro	Leu	Pro	
	530					535					540					
Thr	Ala	Thr	Ser	Met	Ser	Ser	Val	Gly	Met							
545						550										

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Tyr Gly Gly His Tyr Gly Pro Ala Phe Phe Asn His Phe Tyr Glu
1 5 10 15
Gln Asn Glu Arg
20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Ala Ile Gly Val Asn Ile Xaa Tyr Thr Gln Xaa Asn Asn Asp Val
1 5 10 15
Tyr Tyr Ala

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Ala Ile Gly Val Asn Ile Asn Tyr Thr Gln Ser Asn Asn Asp Val
1 5 10 15
Tyr Tyr Ala Phe Gln Gln Thr Gly Asp Phe Val Trp Pro Asn Phe Ile
20 25 30
Glu Asp Leu
35

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Cys Arg Asp Asn Val Glu Gly Pro Xaa Tyr Ala Phe Ala Gly Arg
1 5 10 15

Gly Val Tyr Asp Ile Arg His Pro Tyr Asp Pro Asp Thr
20 25

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TAYGGNGGCA YTAYGGCCNG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATRAARTTGG CCAACRAART C

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Phe	Val	Lys	Asn	Ser	Gly	Ile	Cys	Glu	Thr	Thr	Pro	Gly	Val	Asn	Gln
1				5					10					15	
Tyr	Ser	Gly	Tyr	Leu	Ser	Val	Gly	Ser	Asn	Met	Asn	Met	Trp	Phe	Trp
			20					25					30		
Phe	Phe	Glu	Ala	Arg	Asn	Asn	Pro	Gln	Gln	Ala	Pro	Leu	Ala	Ala	Trp
		35					40					45			
Phe	Asn	Gly	Gly	Pro	Gly	Cys	Ser	Ser	Met	Ile	Gly	Leu	Phe	Gln	Glu
	50					55					60				
Asn	Gly	Pro	Cys	His	Phe	Val	Asn	Gly	Asp	Ser	Thr	Pro	Ser	Leu	Asn
65					70				75					80	
Glu	Asn	Ser	Trp	Asn	Asn	Tyr	Ala	Asn	Met	Ile	Tyr	Ile	Asp	Gln	Pro
				85					90					95	
Ile	Gly	Val	Gly	Phe	Ser	Tyr	Gly	Thr	Asp	Asp	Val	Thr	Ser	Thr	Val
			100					105					110		
Thr	Ala	Ala	Pro	Tyr	Val	Trp	Asn	Leu	Leu	Gln	Ala	Phe	Tyr	Ala	Gln
		115					120					125			
Arg	Pro	Glu	Tyr	Glu	Ser	Arg	Asp	Phe	Ala	Ile	Phe	Thr	Glu	Ser	Tyr
		130				135					140				
Gly	Gly	His	Tyr	Gly	Pro	Glu	Phe	Ala	Ser	Tyr	Ile	Glu	Gln	Gln	Asn
145					150				155					160	
Ala	Ala	Ile	Lys	Ala	Gly	Ser	Val	Thr	Gly	Gln	Asn	Val	Asn	Ile	Val
			165					170						175	
Ala	Leu	Gly	Val	Asn	Asn	Gly	Trp	Ile	Asp	Ser	Thr	Ile	Gln	Glu	Lys
			180					185						190	

Ala	Tyr	Ile	Asp	Phe	Ser	Tyr	Asn	Asn	Ser	Tyr	Gln	Gln	Ile	Ile	Asp
	195						200					205			
Ser	Ser	Thr	Arg	Asp	Ser	Leu	Leu	Asp	Ala	Tyr	Asn	Asn	Gln	Cys	Leu
	210					215					220				
Pro	Ala	Leu	Gln	Gln	Cys	Ser	Gln	Ser	Gly	Ser	Thr	Ser	Asp	Cys	Thr
225					230					235				240	
Asn	Ala	Asp	Ser	Val	Cys	Tyr	Gln	Asn	Ile	Glu	Gly	Pro	Ile	Ser	Ser
			245						250					255	
Ser	Gly	Asp	Phe	Asp	Val	Tyr	Asp	Ile	Arg	Glu	Pro	Ser	Asn	Asp	Pro
		260					265						270		
Tyr	Pro	Pro	Lys	Thr	Tyr	Ser	Thr	Tyr	Leu	Ser	Asp	Pro	Thr	Val	Val
	275						280					285			
Lys	Ala	Ile	Gly	Ala	Arg	Thr	Asn	Tyr	Gln	Glu	Cys	Pro	Asn	Gly	Pro
	290					295					300				
Tyr	Asn	Lys	Phe	Ala	Ser	Thr	Gly	Asp	Asn	Pro	Arg	Ser	Phe	Leu	Ser
305					310					315				320	
Thr	Leu	Ser	Ser	Val	Val	Gln	Ser	Gly	Ile	Asn	Val	Leu	Val	Trp	Ala
				325					330					335	
Gly	Asp	Ala	Asp	Trp	Ile	Cys	Asn	Trp	Leu	Gly	Asn	Tyr	Glu	Val	Ala
		340						345					350		
Asn	Ala	Val	Asp	Phe	Pro	Gly	Asn	Ala	Gln	Phe	Ser	Ala	Leu	Asp	Leu
		355					360					365			
Ala	Pro	Tyr	Thr	Val	Asn	Gly	Val	Glu	Lys	Gly	Gln	Phe	Lys	Thr	Val
	370					375					380				
Asp	Asn	Phe	Ser	Phe	Leu	Lys	Val	Tyr	Gly	Ala	Gly	His	Glu	Val	Pro
385					390					395				400	
Tyr	Tyr	Gln	Pro	Asp	Thr	Ala	Leu	Gln	Ala	Phe	Lys	Gln	Ile	Ile	Gln
				405				410						415	
Lys	Lys	Pro	Ile	Ser	Ser	Thr									
			420												

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ser	Thr	Lys	Asn	Tyr	Arg	Phe	Leu	Asn	Glu	Lys	Thr	Lys	Ala	Asn	Leu
1				5					10					15	
Val	His	His	Leu	Pro	Asp	Val	Pro	Tyr	Asp	Ile	Gly	Glu	Met	Tyr	Ser
			20					25					30		
Gly	Leu	Met	Pro	Ile	Asp	Met	His	Asn	Glu	Ser	Arg	Ala	Leu	Phe	Tyr
		35					40					45			
Ile	Phe	Gln	Pro	Thr	Ile	Gly	Glu	Pro	Val	Asp	Glu	Val	Thr	Ile	Trp
	50					55				60					
Met	Asn	Gly	Gly	Pro	Gly	Cys	Ser	Ser	Met	Glu	Ser	Phe	Leu	Gln	Glu
65					70				75					80	
Thr	Gly	Arg	Phe	Leu	Trp	Gln	Pro	Gly	Thr	Tyr	Ala	Pro	Val	Glu	Asn
			85					90					95		
Pro	Tyr	Ser	Trp	Val	Val	Leu	Thr	Asn	Val	Leu	Trp	Val	Asp	Gln	Pro
		100						105					110		
Val	Gly	Thr	Gly	Tyr	Ser	Ile	Gly	Thr	Pro	Thr	Ala	Thr	Ser	Gln	Glu
		115					120					125			
Glu	Thr	Ala	Gln	Asp	Phe	Val	Lys	Phe	Phe	Lys	Asn	Phe	Gln	Lys	Thr
		130				135					140				
Tyr	Gly	Ile	Lys	Asn	Phe	Lys	Ile	Tyr	Val	Thr	Gly	Glu	Ser	Tyr	Ala
145					150					155				160	
Gly	Arg	Tyr	Val	Pro	Tyr	Ile	Ser	Ala	Ala	Met	Leu	Asp	Glu	Lys	Asp
				165					170					175	
Lys	Glu	Tyr	Phe	Asp	Leu	Gln	Gly	Ala	Leu	Ala	Tyr	Asp	Pro	Cys	Ile
			180					185					190		

Gly	Gln	Phe	Asp	Tyr	Val	Gln	Glu	Glu	Ile	Pro	Val	Val	Pro	Phe	Val
		195					200					205			
Lys	Glu	Asn	Ala	Asn	Leu	Phe	Asn	Phe	Asn	Glu	Thr	Phe	Met	Ala	Glu
	210					215					220				
Leu	Glu	His	Leu	His	Lys	Ser	Cys	Gly	Tyr	Ala	Asp	Phe	Ile	Asp	Lys
225					230					235					240
Tyr	Leu	Thr	Phe	Pro	Pro	Pro	Lys	Glu	Gln	Pro	Pro	Leu	Phe	Phe	Asn
			245						250					255	
Tyr	Thr	Ser	Met	Ala	Asn	Glu	Asp	Val	Phe	Asp	Met	Val	Tyr	Asn	Glu
			260					265					270		
Val	Phe	Lys	Ile	Asn	Pro	Cys	Phe	Asp	Leu	Tyr	Glu	Val	Asn	Leu	Met
		275					280					285			
Cys	Pro	Leu	Gln	Trp	Asp	Val	Leu	Ala	Phe	Pro	Thr	Ser	Leu	Val	Tyr
	290				295						300				
Gln	Pro	Ala	Gly	Ala	Thr	Val	Tyr	Phe	Asp	Arg	Ala	Asp	Val	Lys	Lys
305					310					315					320
Ala	Leu	His	Ala	Pro	Asn	Val	Thr	Trp	Ala	Glu	Cys	Ser	Asn	Asn	Pro
			325						330					335	
Val	Phe	Val	Gly	Gly	Ser	Ser	Gly	Pro	Glu	Gln	Glu	Gly	Asp	Thr	Ser
			340					345					350		
Ala	Asn	Pro	Ile	Glu	His	Val	Leu	Pro	Gln	Val	Ile	Glu	Ala	Thr	Asn
		355					360					365			
Arg	Val	Leu	Ile	Ser	Asn	Gly	Asp	Phe	Asp	Met	Val	Ile	Leu	Thr	Asn
	370					375					380				
Gly	Thr	Leu	Leu	Ala	Ile	Gln	Asn	Met	Thr	Trp	Asn	Gly	His	Leu	Gly
385					390					395					400
Phe	Gln	Lys	Lys	Pro	Ser	Ala	Pro	Ile	Asp	Ile	Lys	Ile	Pro	Asp	Leu
			405						410					415	
Gln	Tyr	Lys	Glu	Val	Phe	Ala	Glu	Asn	Gly	Ala	Ser	Ser	Leu	Asp	Gly
			420					425					430		
Ala	Gln	Gly	Ile	Met	Gly	Val	Gln	His	Tyr	Glu	Arg	Gly	Leu	Met	Lys
		435					440					445			
Ala	Gln	Thr	Tyr	Gln	Ser	Gly	His	Met	Gln	Pro	Gln	Tyr	Gln	Pro	Arg
	450					455					460				
Val	Ala	Tyr	Arg	His	Leu	Glu	Trp	Leu	Leu	Lys	Arg	Thr	Asp	Glu	Leu
465					470					475					480
Gln															

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Arg	Ile	Thr	Ser	Ala	Ile	Ala	Ser	Leu	Leu	Val	Gly	Thr	Ala
1				5					10				15	
Thr	Ser	Leu	Gln	Asn	Pro	His	Arg	Arg	Ala	Val	Pro	Ala	Pro	Leu
			20					25				30		Thr
His	Arg	Ser	Val	Ala	Ser	Arg	Ala	Val	Pro	Val	Glu	Arg	Arg	Ser
		35					40				45			Asn
Asp	Phe	Glu	Tyr	Leu	Thr	Asn	Lys	Thr	Ala	Arg	Phe	Leu	Val	Asn
	50					55					60			Gly
Thr	Ser	Ile	Pro	Glu	Val	Asp	Phe	Asp	Val	Gly	Glu	Ser	Tyr	Ala
65					70					75				80
Leu	Leu	Pro	Asn	Thr	Pro	Thr	Gly	Asn	Ser	Ser	Leu	Phe	Phe	Trp
				85				90					95	Phe
Phe	Pro	Ser	Gln	Asn	Pro	Asp	Ala	Ser	Asp	Glu	Ile	Thr	Ile	Trp
			100					105					110	Leu
Asn	Gly	Gly	Pro	Gly	Cys	Ser	Ser	Leu	Asp	Gly	Leu	Leu	Gln	Glu
	115						120				125			Asn
Gly	Pro	Phe	Leu	Trp	Gln	Pro	Gly	Thr	Tyr	Lys	Pro	Val	Pro	Asn
130						135					140			Pro

Tyr Ser Trp Thr Asn Leu Thr Asn Val Val Tyr Ile Asp Gln Pro Ala
 145 150 155 160
 Gly Thr Gly Phe Ser Pro Gly Pro Ser Thr Val Asn Asp Glu Glu Asp
 165 170 175
 Val Ala Ala Gln Phe Asn Ser Trp Phe Lys His Phe Val Asp Thr Phe
 180 185 190
 Asp Leu His Gly Arg Lys Val Tyr Ile Thr Gly Glu Ser Tyr Ala Gly
 195 200 205
 Met Tyr Val Pro Tyr Ile Ala Asp Ala Met Leu Asn Glu Glu Asp Thr
 210 215 220
 Thr Tyr Phe Asn Leu Lys Gly Ile Gln Ile Asn Asp Pro Ser Ile Asn
 225 230 235 240
 Ser Asp Ser Val Met Tyr Ser Pro Ala Val Arg His Leu Asn His
 245 250 255
 Tyr Asn Asn Ile Phe Arg Leu Asn Ser Thr Phe Leu Ser Tyr Ile Asn
 260 265 270
 Gly Lys Ala Asp Lys Cys Gly Tyr Asn Ala Phe Leu Asp Lys Ala Ile
 275 280 285
 Thr Tyr Pro Pro Pro Thr Pro Phe Pro Thr Ala Pro Glu Ile Thr Glu
 290 295 300
 Asp Cys Gln Val Trp Asp Glu Val Val Met Ala Ala Tyr Asp Ile Asn
 305 310 315 320
 Pro Cys Phe Asn Tyr Tyr His Leu Ile Asp Phe Cys Pro Tyr Leu Trp
 325 330 335
 Asp Val Leu Gly Phe Pro Ser Leu Gly Phe Gly Pro Asp Asn Tyr Phe
 340 345 350
 Asn Arg Ser Asp Val Gln Lys Ile Leu His Val Pro Pro Thr Asp Tyr
 355 360 365
 Ser Val Cys Ser Glu Thr Val Ile Phe Ala Asn Gly Asp Gly Ser Asp
 370 375 380
 Pro Ser Ser Trp Gly Pro Leu Pro Ser Val Ile Glu Arg Thr Asn Asn
 385 390 395 400
 Thr Ile Ile Gly His Gly Trp Leu Asp Tyr Leu Leu Phe Leu Asn Gly
 405 410 415
 Ser Leu Ala Thr Ile Gln Asn Met Thr Trp Asn Gly Lys Gln Gly Phe
 420 425 430
 Gln Ser Pro Val Glu Pro Leu Phe Val Pro Tyr His Tyr Gly Leu
 435 440 445
 Ala Glu Leu Tyr Trp Gly Asp Glu Pro Asp Pro Tyr Asn Leu Asp Ala
 450 455 460
 Gly Ala Gly Tyr Leu Gly Thr Ala His Thr Glu Arg Gly Leu Thr Phe
 465 470 475 480
 Ser Ser Val Tyr Leu Ser Gly His Glu Ile Pro Gln Tyr Val Pro Gly
 485 490 495
 Ala Leu Thr Ala Ser Trp Ser Ser Cys Leu Val Glu Leu Ile Val Phe
 500 505 510
 Pro Arg Arg Gly Thr Thr Pro Leu Asn Phe Ser
 515 520

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 530 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Leu Phe Arg Ser Leu Leu Ser Thr Ala Val Leu Ala Val Ser Leu
 1 5 10 15
 Cys Thr Asp Asn Ala Ser Ala Ala Lys His Gly Arg Phe Gly Gln Lys
 20 25 30
 Ala Arg Asp Ala Met Asn Ile Ala Asn Gly Ser Ala Asn Ala Val Lys
 35 40 45

His	Ser	Leu	Lys	Ile	Pro	Val	Glu	Asp	Tyr	Gln	Phe	Leu	Asn	Asn	Lys
50						55					60				
Thr	Lys	Pro	Tyr	Arg	Val	Glu	Ser	Leu	Pro	Asp	Val	His	Phe	Asp	Leu
65					70					75					80
Gly	Glu	Met	Tyr	Ser	Gly	Leu	Val	Pro	Ile	Glu	Lys	Gly	Asn	Val	Ser
				85					90					95	
Arg	Ser	Leu	Phe	Phe	Val	Phe	Gln	Pro	Thr	Ile	Gly	Glu	Pro	Val	Asp
			100					105					110		
Glu	Thr	Thr	Ile	Trp	Leu	Asn	Gly	Gly	Pro	Gly	Cys	Ser	Ser	Leu	Glu
		115					120					125			
Ala	Leu	Ser	Pro	Gly	Glu	Cys	Arg	Phe	Val	Trp	Gln	Pro	Gly	Thr	Tyr
	130						135				140				
Gln	Pro	Val	Glu	Asn	Pro	Tyr	Ser	Trp	Val	Asn	Leu	Thr	Asn	Val	Leu
145					150					155					160
Trp	Val	Asp	Gln	Pro	Val	Gly	Thr	Gly	Phe	Ser	Leu	Gly	Val	Pro	Thr
				165					170					175	
Ala	Thr	Ser	Glu	Glu	Ile	Ala	Glu	Asp	Phe	Val	Lys	Phe	Phe	Lys	
			180					185					190		
Asn	Trp	Gln	Gln	Ile	Phe	Gly	Ile	Lys	Asn	Phe	Lys	Ile	Tyr	Val	Thr
		195					200					205			
Gly	Glu	Ser	Tyr	Ala	Gly	Arg	Tyr	Val	Pro	Tyr	Ile	Ser	Ala	Ala	Phe
	210					215					220				
Leu	Asp	Gln	Asn	Asp	Thr	Glu	His	Phe	Asn	Leu	Lys	Gly	Ala	Leu	Ala
225					230					235					240
Tyr	Asp	Pro	Cys	Ile	Gly	Gln	Phe	Asp	Tyr	Val	Gln	Glu	Glu	Ala	Pro
				245					250					255	
Val	Val	Pro	Phe	Val	Gln	Lys	Asn	Asn	Ala	Leu	Phe	Asn	Phe	Asn	Ala
			260					265					270		
Ser	Phe	Leu	Ala	Glu	Leu	Glu	Ser	Ile	His	Glu	Gln	Cys	Gly	Tyr	Lys
		275					280					285			
Asp	Phe	Ile	Asp	Gln	Tyr	Leu	Val	Phe	Pro	Ala	Ser	Gly	Val	Gln	Pro
	290					295					300				
Pro	Lys	Ala	Met	Asn	Trp	Ser	Asp	Pro	Thr	Cys	Asp	Val	Tyr	Asp	Ile
305					310					315					320
Val	Asn	Asn	Ala	Val	Leu	Asp	Pro	Asn	Pro	Cys	Phe	Asn	Pro	Tyr	Glu
				325					330					335	
Ile	Asn	Glu	Met	Cys	Pro	Ile	Leu	Trp	Asp	Val	Leu	Gly	Phe	Pro	Thr
		340						345					350		
Glu	Val	Asp	Tyr	Leu	Pro	Ala	Ala	Pro	Ala	Ser	Thr	Leu	Thr	Ala	Leu
		355					360					365			
Ile	Lys	Arg	Ala	Met	His	Ala	Pro	Asn	Ile	Thr	Trp	Ser	Glu	Cys	Ser
	370					375					380				
Val	Glu	Ser	Val	Phe	Val	Gly	Gly	Asp	Gly	Gly	Pro	Glu	Gln	Glu	Gly
385					390					395					400
Asp	Tyr	Ser	Ala	Asn	Pro	Ile	Glu	His	Val	Leu	Pro	Gln	Val	Ile	Glu
				405					410					415	
Gly	Thr	Asn	Arg	Val	Leu	Ile	Gly	Asn	Gly	Asp	Tyr	Asp	Met	Val	Ile
			420					425					430		
Leu	Thr	Asn	Gly	Thr	Leu	Leu	Ser	Ile	Gln	Asn	Met	Thr	Trp	Asn	Gly
		435					440					445			
Lys	Leu	Gly	Phe	Asp	Thr	Ala	Pro	Ser	Thr	Pro	Ile	Asn	Ile	Asp	Ile
	450					455					460				
Pro	Asp	Leu	Met	Tyr	Asn	Glu	Val	Phe	Ile	Glu	Asn	Gly	Tyr	Asp	Pro
465					470					475					480
Gln	Gly	Gly	Gln	Gly	Val	Met	Gly	Ile	Gln	His	Tyr	Glu	Arg	Gly	Leu
				485					490					495	
Met	Trp	Ala	Glu	Thr	Phe	Gln	Ser	Gly	His	Met	Gln	Pro	Gln	Phe	Gln
		500						505					510		
Pro	Arg	Val	Ser	Tyr	Arg	His	Leu	Glu	Trp	Leu	Leu	Gly	Arg	Arg	Asp
		515					520					525			
Thr	Leu														
	530														